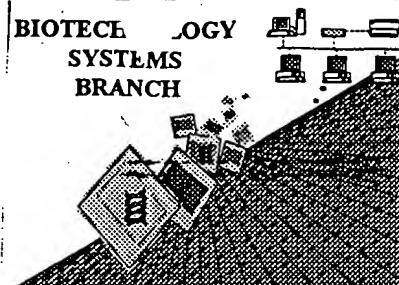


**BEST AVAILABLE COPY**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**



028c

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/676,249

Source: OIPE

Date Processed by STIC: 10-10-00

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Sequence Listing Error Summary

127

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/676,249

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES)      Sequence(s) \_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 10/10/2000

PATENT APPLICATION: US/09/676,249

TIME: 16:31:41

Input Set : A:\PC10555A-SEQ-LIST.txt

Output Set: N:\CRF3\10102000\I676249.raw

4 <110> APPLICANT: King, Kendall W  
 5 Madura, Rebecca A  
 6 Rosey, Everett L  
 8 <120> TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA PNEUMONIAE  
 9 mhp3 GENE AND USES THEREOF  
 11 <130> FILE REFERENCE: PC10555  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/676,249  
 C--> 14 <141> CURRENT FILING DATE: 2000-09-29  
 15 <150> PRIOR APPLICATION NUMBER: US 60/156,602  
 16 <151> PRIOR FILING DATE: 1999-09-29  
 18 <160> NUMBER OF SEQ ID NOS: 41  
 20 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply  
 Corrected Diskette Needed  
 see PP. 1, 2, 3

## ERRORED SEQUENCES

153 <210> SEQ ID NO: 3  
 154 <211> LENGTH: 1263  
 155 <212> TYPE: DNA  
 156 <213> ORGANISM: Artificial Sequence  
 158 <220> FEATURE:  
 159 <223> OTHER INFORMATION: Description of Artificial Sequence: mhp3  
 160 manipulated for in vitro expression  
 162 <400> SEQUENCE: 3  
 163 atgtgggata aagaaacaac taaagaagaa aaatcagccg ataatacaaaa taagcaaatac 60  
 164 actgatgtct caaaaatttc aggactagtt aatgaacgaa aatccgaaat tatggccgca 120  
 165 aaagctgatg caaacaaaca ttttgggcta aatatggcaa ttgtaaccgc tggtggaacg 180  
 166 gtaaatgata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt 240  
 167 actggagggt agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 300  
 168 tcacttgcta ataccaacaa aaatgtttgg gtactttctg gttttcaaca cgggtgatgcg 360  
 169 ttcacaagat gggttaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc 420  
 170 atactcggaa ttgactggac tgatactgaa aatgtaattc caacaggctc atataattaat 480  
 171 ttaacctata aaactgaaga agccggatgg cttgcaggat atgcgaatgc ttcctttttg 540  
 172 gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tggtgggatt 600  
 173 tcgccagctg taactgattt tatcgtggtt tatctagccg gaattaaagc ttggaatcta 660  
 174 aaaaattctg ataaaaaaac aaagataaca actgataaaa tcgagataaa tcttggggtt 720  
 175 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 780  
 176 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcgatat aatcgcaaac 840  
 177 caaatgatac gttatctcat tgggtgtgac accgaccaat cacttgttta tacaaaaact 900  
 178 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt 960  
 179 agtgatttat ataccaaaaa atcaaattca agaaatttag cgggctttga atttggtaaa 1020  
 180 aaaagtgcac ccgtttatct tgggaattaaa gacagggttg tcgatattgc tgatacttct 1080  
 181 ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt 1140  
 182 gaagaaaaaa ctaagacaat tcctgccgaa gaagttcgta aaactttaga aattccggaa 1200  
 183 atgcctgata aacaacctga taagcaacag gaaagcttag acaaaactaat taccgatatt 1260  
 E--> 184 aataatcta 1263

Number of bases  
 conflict:

1263 listed  
 1269 shown

09/676, 249

P. 2

<210> 7  
<211> 14  
<212> PRT  
<213> Mycoplasma hyopneumoniae

<400> 7  
Ala Gly (Xaa) Trp Ala Lys Glu Thr Thr Lys Glu Glu Lys Ser  
1 5 10

Missing mandatory <220> to <223> features  
to explain "Xaa" in sequence. See #10  
on Error Summary Sheet.

09/676, 249

P. 3

<210> 10  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 10  
tgytgrg~~na~~ argara~~na~~c~~na~~argargar

30

Missing mandatory <220> to <223> features  
to explain "n's" in sequence. See #10  
on Error Summary Sheet.



**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 10/10/2000

PATENT APPLICATION: US/09/676,249

TIME: 16:31:43

Input Set : A:\PC10555A-SEQ-LIST.txt

Output Set: N:\CRF3\10102000\I676249.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:184 M:254 E: No. of Bases conflict, LENGTH:Input:1263 Counted:1269 SEQ:3  
L:184 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1263 Found:1269 SEQ:3  
L:275 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:275 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:275 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4  
L:350 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:350 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7  
L:350 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:350 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:350 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7  
L:395 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:395 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:395 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10  
L:421 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:421 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:421 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12  
L:447 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14  
L:447 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:447 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14